

*F. Hamed*

## **RAW SEQUENCE LISTING ERROR REPORT**

BIOTECHNOLOGY  
SYSTEMS  
BRANCH

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OCT 17 2000

TECH CENTER 1600/2900

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/265,540B

Source: 1643

Date Processed by STIC: 10/2/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin30help@uspto.gov](mailto:patin30help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER  
VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW:

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

1643

## RAW SEQUENCE LISTING

DATE: 10/02/2000

PATENT APPLICATION: US/09/265,540B

TIME: 10:47:24

Input Set : A:\804Krvs2.txt

Output Set: N:\CRF3\09292000\I265540B.raw

Does Not Comply  
Corrected Diskette Needed

3 <110> APPLICANT: Parham, Christi L.  
 4 Moore, Kevin W.  
 5 Murgolo, Nicholas J.  
 6 Bazan, J. Fernando  
 8 <120> TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods  
 10 <130> FILE REFERENCE: DX0804  
 12 <140> CURRENT APPLICATION NUMBER: US/09/265,540B  
 13 <141> CURRENT FILING DATE: 1999-03-08  
 15 <160> NUMBER OF SEQ ID NOS: 6  
 17 <170> SOFTWARE: PatentIn Ver. 2.0  
 19 <210> SEQ ID NO: 1  
 20 <211> LENGTH: 1381  
 21 <212> TYPE: DNA  
 22 <213> ORGANISM: primate  
 24 <220> FEATURE:  
 25 <221> NAME/KEY: CDS  
 26 <222> LOCATION: (132)..(1064)  
 28 <220> FEATURE:  
 29 <221> NAME/KEY: misc\_feature  
 30 <222> LOCATION: n at position 567 and 573  
 31 <223> OTHER INFORMATION: n may be A, C, T, or G; translated amino acid depends on genetic code  
 33 <400> SEQUENCE: 1  
 34 tcgacccacg cgtccgcgt gcgactcaga cctcagctcc aacatatgca ttctgaagaa 60  
 36 agatggctga gatggacaga atgctttatt ttggaaagaa acaatgttct aggtcaaaact 120  
 38 gagtctacca a atg cag act ttc aca atg gtt cta gaa gaa atc tgg aca 170  
 39 Met Gln Thr Phe Thr Met Val Leu Glu Glu Ile Trp Thr  
 40 1 5 10  
 42 agt ctt ttc atg tgg ttt ttc tac gca ttg att cca tgt ttg ctc aca 218  
 43 Ser Leu Phe Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr  
 44 15 20 25  
 46 gat gaa gtg gcc att ctg cct gcc cct cag aac ctc tct gta ctc tca 266  
 47 Asp Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser  
 48 30 35 40 45  
 50 acc aac atg aag cat ctc ttg atg tgg agc cca gtg atc gcg cct gga 314  
 51 Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly  
 52 50 55 60  
 54 gaa aca gtg tac tat tct gtc gaa tac cag ggg gag tac gag agc ctg 362  
 55 Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu Ser Leu  
 56 65 70 75  
 58 tac acg agc cac atc tgg atc ccc agc agc tgg tgc tca ctc act gaa 410  
 59 Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu  
 60 80 85 90  
 62 ggt cct gag tgt gat gtc act gat gac atc acg gcc act gtg cca tac 458  
 63 Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr  
 64 95 100 105  
 66 aac ctt cgt gtc agg gcc aca ttg ggc tca cag acc tca gcc tgg agc 506  
 67 Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser

what about n's at positions 1336, 1342, 1369?  
 (P.2)

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Input Set : A:\804Krvs2.txt

Output Set : N:\CRF3\09292000\I265540B.raw

```

68 110          115          120          125
70 atc ctg aag cat ccc ttt aat aga aac tca acc atc ctt acc cga cct 554
71 Ile Leu Lys His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro
72          130          135          140
W--> 74 ggg atg gag atc ncc aaa nat ggc ttc cac ctg gtt att gag ctg gag 602
W- 75 Gly Met Glu Ile Xaa Lys Xaa Gly Phe His Leu Val Ile Glu Leu Glu
76          145          150          155
78 gac ctg ggg ccc cag ttt gag ttc ctt gtg gcc tac tgg asg agg gag 650
W- 79 Asp Leu Gly Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Xaa Arg Glu
80          160          165          170
82 cct ggt gcc gag gaa cat gtc aaa atg gtg agg agt ggg ggt att cca 698
83 Pro Gly Ala Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro
84          175          180          185
86 gtg cac cta gaa acc atg gag cca ggg gct gca tac tgt gtg aag gcc 746
87 Val His Leu Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala
88 190          195          200          205
W- 90 cag aca ttc gtg aag gcc att ggg arg tac agc gcc ttc agc cag aca 794
W- 91 Gln Thr Phe Val Lys Ala Ile Gly Xaa Tyr Ser Ala Phe Ser Gln Thr
92          210          215          220
W- 94 gaa tgt gtg gar gtg caa gga gag gcc att ccc ctg gta ctg gcc ctg 842
W- 95 Glu Cys Val Xaa Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu
96          225          230          235
98 ttt gcc ttt gtt ggc ttc atg ctg atc ctt gtg gtc gtg cca ctg ttc 890
99 Phe Ala Phe Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe
100          240          245          250
102 gtc tgg aaa atg ggc cgg ctg ctc cag tac tcc tgt tgc ccc gtg gtg 938
103 Val Trp Lys Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val
104          255          260          265
106 gtc ctc cca gac acc ttg aaa ata acc aat tca ccc cag aag tta atc 986
107 Val Leu Pro Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile
108 270          275          280          285
110 agc tgc aga agg gag gag gtg gat gcc tgt gcc acg gct gtg atg tct 1034
111 Ser Cys Arg Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met Ser
112          290          295          300
114 cct gag gaa ctc ctc agg gcc tgg atc tca taggtttgag gaagggccca 1084
115 Pro Glu Glu Leu Leu Arg Ala Trp Ile Ser
116          305          310
118 ggtgaagccg agaacctggt ctgcatgaca tggaaacct gaggggacaa gttgtgtttc 1144
120 tgttttccgc caggacaag gtagtagaga agtaggaaga gcctgttgc tacaagtcta 1204
122 gaagcaacca tcagaggcag ggtggtttgt ckaacagaac aaytgactga ggytakrggg 1264
124 gwtgtgacct cagactktg ggstkscayt tgcwtggytg agcaacctg gaaaaagtga 1324
W--> 126 cttcatccct tgggtcccaa gttttctcat ctgtaatggg ggatccctac aaaactg 1381
129 <210> SEQ ID NO: 2
130 <211> LENGTH: 311
131 <212> TYPE: PRT
132 <213> ORGANISM: primate
134 <220> FEATURE:
135 <221> NAME/KEY: misc_feature / / / / /
136 <222> LOCATION: Xaa at residues 146, 148, 171, 214 and 225

```

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Output Set: N:\CRF3\09292000\I265540B.raw

137 <223> OTHER INFORMATION: Xaa depends on corresponding codon  
 139 <400> SEQUENCE: 2  
 140 Met Gln Thr Phe Thr Met Val Leu Glu Glu Ile Trp Thr Ser Leu Phe  
 141 1 5 10 15  
 143 Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr Asp Glu Val  
 144 20 25 30  
 146 Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser Thr Asn Met  
 147 35 40 45  
 149 Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly Glu Thr Val  
 150 50 55 60  
 152 Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu Ser Leu Tyr Thr Ser  
 153 65 70 75 80  
 155 His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu Gly Pro Glu  
 156 85 90 95  
 158 Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr Asn Leu Arg  
 159 100 105 110  
 161 Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser Ile Leu Lys  
 162 115 120 125  
 164 His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro Gly Met Glu  
 165 130 135 140  
 W--> 167 Ile Xaa Lys Xaa Gly Phe His Leu Val Ile Glu Leu Glu Asp Leu Gly  
 168 145 150 155 160  
 W--> 170 Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Xaa Arg Glu Pro Gly Ala  
 171 165 170 175  
 173 Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro Val His Leu  
 174 180 185 190  
 176 Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala Gln Thr Phe  
 177 195 200 205  
 W--> 179 Val Lys Ala Ile Gly Xaa Tyr Ser Ala Phe Ser Gln Thr Glu Cys Val  
 180 210 215 220  
 W--> 182 Xaa Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu Phe Ala Phe  
 183 225 230 235 240  
 185 Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe Val Trp Lys  
 186 245 250 255  
 188 Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val Val Leu Pro  
 189 260 265 270  
 191 Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile Ser Cys Arg  
 192 275 280 285  
 194 Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met Ser Pro Glu Glu  
 195 290 295 300  
 197 Leu Leu Arg Ala Trp Ile Ser  
 198 305 310  
 201 <210> SEQ ID NO: 3  
 202 <211> LENGTH: 1244  
 203 <212> TYPE: DNA  
 204 <213> ORGANISM: primate  
 206 <220> FEATURE:  
 207 <221> NAME/KEY: CDS  
 208 <222> LOCATION: (2)..(694)

## RAW SEQUENCE LISTING

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TIME: 10:47:24

Input Set : A:\804Krvs2.txt

Output Set: N:\CRF3\09292000\I265540B.raw

210 <400> SEQUENCE: 3  
 211 c cgg gtc gac cca cgc gtc cgc ctg gtt tcc ccc tgg ctg aca gtg cct 49  
 212 Arg Val Asp Pro Arg Val Arg Leu Val Ser Pro Trp Leu Thr Val Pro  
 213 1 5 10 15  
 215 tgg ttc ctg tcc tgt tgg aat gtt acc att ggg cct cct gag agc atc 97  
 216 Trp Phe Leu Ser Cys Trp Asn Val Thr Ile Gly Pro Pro Glu Ser Ile  
 217 20 25 30  
 219 tgg gtg acg cgg gga gaa gcc tcc ctc atc atc agg ttc tcc tct ccc 145  
 220 Trp Val Thr Pro Gly Glu Ala Ser Leu Ile Ile Arg Phe Ser Ser Pro  
 221 35 40 45  
 223 ttc gac gtc cct ccc aac ctg ggc tat ttc cag tac tat gtc cat tay 193  
 224 Phe Asp Val Pro Pro Asn Leu Gly Tyr Phe Gln Tyr Tyr Val His Xaa  
 225 50 55 60  
 227 tgg gaa aag gcg gga atc caa aag gtt aaa ggt cct ttc aag agc aac 241  
 228 Trp Glu Lys Ala Gly Ile Gln Lys Val Lys Gly Pro Phe Lys Ser Asn  
 229 65 70 75 80  
 231 tcc atc gtg ttg gat ggc ttg aga ccc tta aga gaa tac tgt tta caa 289  
 232 Ser Ile Val Leu Asp Gly Leu Arg Pro Leu Arg Glu Tyr Cys Leu Gln  
 233 85 90 95  
 235 gtg aag gcg cat ctc ttt cgc aca tcc tgc aac acc tct agg ccc ggc 337  
 236 Val Lys Ala His Leu Phe Arg Thr Ser Cys Asn Thr Ser Arg Pro Gly  
 237 100 105 110  
 239 cgc tta agc aac ata act tgc tac gaa aca atg atg gat gcc act acg 385  
 240 Arg Leu Ser Asn Ile Thr Cys Tyr Glu Thr Met Met Asp Ala Thr Thr  
 241 115 120 125  
 243 aag ctt caa caa gtc atc ctc atc gcc gtg gga gtc ttt ctg tcg ctg 433  
 244 Lys Leu Gln Gln Val Ile Leu Ile Ala Val Gly Val Phe Leu Ser Leu  
 245 130 135 140  
 247 gcg gcg ctg gcg ggg ggc tgt ttc ttc ctg gtg ctg aga tac aaa ggc 481  
 248 Ala Ala Leu Ala Gly Gly Cys Phe Phe Leu Val Leu Arg Tyr Lys Gly  
 249 145 150 155 160  
 251 ctg gtg aaa tac tgg ttt cac tct ccg cca agc atc cca tca caa atc 529  
 252 Leu Val Lys Tyr Trp Phe His Ser Pro Pro Ser Ile Pro Ser Gln Ile  
 253 165 170 175  
 255 gaa gag tat ctg aag gac ccg agc cag cct atc cta gag gcc ctg gac 577  
 256 Glu Glu Tyr Leu Lys Asp Pro Ser Gln Pro Ile Leu Glu Ala Leu Asp  
 257 180 185 190  
 259 aag gac acg tca cca aca gat gat gcc tgg gac ttg gtg tct gtt gtt 625  
 260 Lys Asp Thr Ser Pro Thr Asp Asp Ala Trp Asp Leu Val Ser Val Val  
 261 195 200 205  
 263 gca ttt cca gca aag gag caa gaa gat gtt ccc caa agc act ttg acc 673  
 264 Ala Phe Pro Ala Lys Glu Gln Glu Asp Val Pro Gln Ser Thr Leu Thr  
 265 210 215 220  
 267 caa aac tct ggt gcg gtc tgc tagcctgtgg ggtaagggt ctgagccgag 724  
 268 Gln Asn Ser Gly Ala Val Cys  
 269 225 230  
 271 gaagctgctg atgtccatgt cagcaattta tggaaatccg tccatccattt tccgtgtccc 784  
 273 aaaaggcccg tcagtgccctg tgaagatgta acgggtctca tgggggacac aagcttattg 844  
 275 atttttttct tcaactaag agttttctaa tcatacgcgt ttttagaata attctacaga 904

## RAW SEQUENCE LISTING

DATE: 10/02/2000

PATENT APPLICATION: US/09/265,540B

TIME: 10:47:24

Input Set : A:\804Krvs2.txt

Output Set: N:\CRF3\09292000\I265540B.raw

277 tatgtcccg aaagattaag atttctctta aactactaaa agacatgtaa ttatttgta 964  
 279 gcaaatggg gtctggcagc cctctgacac ttttctgtca gcagccagga cagcaggtcc 1024  
 281 cctccttgat gaagccctc ggcagacca tgtcacctgt ccagcctgc cccaagaagg 1084  
 283 gacattaagt ggccttctt catatccaaa cactggctt gaaatgtgat tagccctgta 1144  
 285 aatagtttca cagagattaa gcctttttt cccccaagt aggaataaaa gactataatt 1204  
 287 aactttttta aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1244  
 290 <210> SEQ ID NO: 4  
 291 <211> LENGTH: 231  
 292 <212> TYPE: PRT  
 293 <213> ORGANISM: primate  
 295 <220> FEATURE:  
 296 <221> NAME/KEY: misc\_feature  
 297 <222> LOCATION: Xaa at residue 64  
 298 <223> OTHER INFORMATION: Xaa translated amino acid depends on corresponding codon  
 300 <400> SEQUENCE: 4  
 301 Arg Val Asp Pro Arg Val Arg Leu Val Ser Pro Trp Leu Thr Val Pro  
 302 1 5 10 15  
 304 Trp Phe Leu Ser Cys Trp Asn Val Thr Ile Gly Pro Pro Glu Ser Ile  
 305 20 25 30  
 307 Trp Val Thr Pro Gly Glu Ala Ser Leu Ile Ile Arg Phe Ser Ser Pro  
 308 35 40 45  
 310 Phe Asp Val Pro Pro Asn Leu Gly Tyr Phe Gln Tyr Tyr Val His Xaa  
 311 50 55 60  
 313 Trp Glu Lys Ala Gly Ile Gln Lys Val Lys Gly Pro Phe Lys Ser Asn  
 314 65 70 75 80  
 316 Ser Ile Val Leu Asp Gly Leu Arg Pro Leu Arg Glu Tyr Cys Leu Gln  
 317 85 90 95  
 319 Val Lys Ala His Leu Phe Arg Thr Ser Cys Asn Thr Ser Arg Pro Gly  
 320 100 105 110  
 322 Arg Leu Ser Asn Ile Thr Cys Tyr Glu Thr Met Met Asp Ala Thr Thr  
 323 115 120 125  
 325 Lys Leu Gln Gln Val Ile Leu Ile Ala Val Gly Val Phe Leu Ser Leu  
 326 130 135 140  
 328 Ala Ala Leu Ala Gly Gly Cys Phe Phe Leu Val Leu Arg Tyr Lys Gly  
 329 145 150 155 160  
 331 Leu Val Lys Tyr Trp Phe His Ser Pro Pro Ser Ile Pro Ser Gln Ile  
 332 165 170 175  
 334 Glu Glu Tyr Leu Lys Asp Pro Ser Gln Pro Ile Leu Glu Ala Leu Asp  
 335 180 185 190  
 337 Lys Asp Thr Ser Pro Thr Asp Asp Ala Trp Asp Leu Val Ser Val Val  
 338 195 200 205  
 340 Ala Phe Pro Ala Lys Glu Gln Glu Asp Val Pro Gln Ser Thr Leu Thr  
 341 210 215 220  
 343 Gln Asn Ser Gly Ala Val Cys  
 344 225 230  
 347 <210> SEQ ID NO: 5  
 348 <211> LENGTH: 337  
 349 <212> TYPE: PRT  
 350 <213> ORGANISM: primate

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/265,540B

DATE: 10/02/2000  
TIME: 10:47:25

Input Set : A:\804Krvs2.txt  
Output Set: N:\CRF3\09292000\I265540B.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:74 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:75 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:79 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:91 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:95 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:126 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:167 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:170 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:179 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:182 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:224 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3  
L:224 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:3  
L:310 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING  
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 CFR 1.821-1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 CFR 1.821.825. Applicant's attention is directed to these regulations, published at 114 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 CFR 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 CFR 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, as indicated on the attached copy of marked-up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A substitute computer readable form must be submitted as required by 37 CFR 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 CFR 1.821(e).
- ☐ 7. Other: \_\_\_\_\_

**Applicant must provide:**

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing"
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 CFR 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d)

For questions regarding compliance with these requirements, please contact

For Rules Interpretation, call (703) 308-1123  
For CRF submission help, call (703) 308-4212  
For PatentIn software help, call (703) 557-0400

Please return a copy of this notice with your response.